



Seq\_listing\_US\_korrigiert141102.txt  
SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH; Marina Vrlijc et al.

<120> Process for the microbial production of amino acids by  
boosted activity of export carriers

<130> 1

<140> US/09/105,117 PCT/DE96/02485

<141> 1998-06-17

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220> (LySE)

<221> gene

<222> CDS (1016)..(1726)

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gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240
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cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360
acgggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcatcgag cccaatctag 420
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taaaacatct ccacgccgca gcaaggataa tgtgtgcgct tcatcttcca agcgcagcgt 600
gagcgttgct ccacccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660
cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttagcg 720
tttagtttct gcttgacgca acaccatttt ccgcgctgct tgcacaagga cttcaccgcg 780
ttcggttgct ttggccggtt ggggtgcgca taccaacact cgaccacgt gatgctcgag 840
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gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatggggt tcatgaagct 960
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tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114  
Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile  
20 25 30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162  
Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp  
35 40 45

gtc ttt ttg ttc atc gcc gcc acc ttg gcc gtt gat ctt ttg tcc aat 1210  
Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn  
50 55 60 65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt gcc atc gct tac 1258  
Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr  
70 75 80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306  
Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys  
85 90 95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354  
Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp  
100 105 110

gac acg cct ttg gcc ggt tcg gcg gtg gcc act gac acg cgc aac cgg 1402  
Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg  
115 120 125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450  
Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro  
130 135 140 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498  
Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu  
150 155 160

gac gcg ttt gtg ttt atc gcc gcc gtc gcc gcg caa tac gcc gac acc 1546  
Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr  
165 170 175

gga cgg tgg att ttc gcc gct gcc gcg ttc gcg gca agc ctg atc tgg 1594  
Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp  
180 185 190

ttc ccg ctg gtg ggt ttc gcc gca gca gca ttg tca cgc ccg ctg tcc 1642  
Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser  
195 200 205

agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690  
Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met  
210 215 220 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736  
Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly  
230 235

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tcgcctccaa ctcggcgctca gaaaactcca agttgttgag tgaatcaagg ctgttgtcca 1856  
gctgctcaac tgacgaagca ccaatcaatg cactgggtcac ggtatccgag ccgtactctc 1916  
cttgctcgag cagcaccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976  
cgatgtcatt gagcttgagg accatatcaa tattgttcac gttcaacatg ccctcagaca 2036  
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gcaggccctg cgcaagtggg gagaaagcaa tgacgccaag accattgttg gcagctgact 2156  
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<220> (LySE)

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20 25 30  
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser  
35 40 45  
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser  
50 55 60  
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala  
65 70 75 80  
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn  
85 90 95  
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro  
100 105 110  
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn  
115 120 125  
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys  
130 135 140  
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr  
145 150 155 160  
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp  
165 170 175

## Seq\_listing\_US\_korrigiert141102.txt

Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile  
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 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu  
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 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val  
 210 215 220  
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 <220> (complement to <210> 1)  
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 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc 97  
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu  
 20 25 30  
 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145  
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu  
 35 40 45  
 att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg 193  
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro  
 50 55 60  
 ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241  
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu  
 65 70 75 80  
 ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa 289  
 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys  
 85 90 95  
 tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337  
 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser  
 100 105 110  
 ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag 385  
 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys  
 115 120 125  
 ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg 433

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ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg			481
Leu Ala Trp Val Leu Arg	Glu Gln Gly Glu Tyr	Gly Ala Asp Thr Val	
145	150	155	160
acc agt gca ttg att ggt gct tct tca gtt gag cag ctg gac aac agc			529
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser			
	165	170	175
ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg			577
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala			
	180	185	190
atc gat gag att tcc cac gac gcc gcc atc aac att tgg gcg aag gcc			625
Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala			
	195	200	205
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Thr Asp Ser Lys Thr Arg Glu Asn			
	210	215	
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tgccgcgaac gcgccagcg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac			852
gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat			912
tgccatcaac atgggcttta cccaaacccg ctgcttatcg acgctcacct ccacccgcac			972
ccggttgcg gtgtcagtgg ccaccgccga accgccc aaa ggcgtgtcat cgggcacggt			1032
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tgccatgacg gcaaaccata acaggttaagc gatgccaccc cagcgcataa tatcgagcac			1152
gatcggcgcg gcattggaca aaagatcaac gcccaagggtg ccggcgatga acaaaaagac			1212
gtcagaaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttgttt			1272
aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggcccca aaagcagacc			1332
tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt			1392
ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act			1444
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ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc			1492
Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala			
	230	235	240
ctt tcc att tcc ccc tct gcg gtg agt cag cgc gtt aaa gct ctc gag			1540
Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu			
	245	250	255
cat cac gtg ggt cga gtg ttg gta tct cgc acc caa ccg gcc aaa gca			1598
His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala			
	260	265	270

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ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc	1684
Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile	
290 295 300 305	
ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct	1732
Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro	
310 315 320	
ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg	1780
Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu	
325 330 335	
cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat	1828
Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp	
340 345 350	
gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa	1876
Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu	
355 360 365	
gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca	1924
Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser	
370 375 380 385	
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Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met	
390 395 400	
ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg	2020
Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu	
405 410 415	
gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc	2068
Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val	
420 425 430	
ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg	2116
Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp	
435 440 445	
gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa	2164
Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu	
450 455 460 465	
gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa	2212
Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln	
470 475 480	
cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc	2260
Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val	
485 490 495	
gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag	2313
Val Asp Ala Ala Ile Glu Gly Leu Arg Pro	
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2374

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 35 40 45  
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro  
 50 55 60  
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu  
 65 70 75 80  
 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys  
 85 90 95  
 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser  
 100 105 110  
 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys  
 115 120 125  
 Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala  
 130 135 140  
 Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val  
 145 150 155 160  
 Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser  
 165 170 175  
 Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala  
 180 185 190  
 Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala  
 195 200 205  
 Thr Asp Ser Lys Thr Arg Glu Asn  
 210 215

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 <220> (LysG)

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25

30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val  
 35 40 45  
 Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val  
 50 55 60  
 Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln  
 65 70 75 80  
 Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala  
 85 90 95  
 Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser  
 100 105 110  
 Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr  
 115 120 125  
 Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu  
 130 135 140  
 Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg  
 145 150 155 160  
 His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp  
 165 170 175  
 Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys  
 180 185 190  
 Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val  
 195 200 205  
 Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu  
 210 215 220  
 Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala  
 225 230 235 240  
 Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro  
 245 250 255  
 Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser  
 260 265 270  
 Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu  
 275 280 285  
 Arg Pro  
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